



## SEQUENCE LISTING

<110> National Institute of Advanced Industrial Science and  
Technology  
ISHIKAWA, Kazuhiko  
JOEN, Sung-Jong

<120> HEAT-RESISTANT DNA LIGASE

<130> Q79424

<140> 10/780,731

<141> 2004-02-19

<150> JP 2003-045224

<151> 2003-02-24

<160> 7

<170> PatentIn version 3.3

<210> 1

<211> 1860

<212> DNA

<213> Aeropyrum pernix

<220>

<221> CDS

<222> (1) .. (1860)

<400> 1

gtg ggg tgt ctg gtt ttg gct tct agc tct ggg ggt gtt gga ggc ggt	48
Val Gly Cys Leu Val Leu Ala Ser Ser Ser Gly Gly Val Gly Gly Gly	
1 5 10 15	
gac atg cct ttc aag ccc gtg gct gag gcc ttc gcc tcc atg gag agg	96
Asp Met Pro Phe Lys Pro Val Ala Glu Ala Phe Ala Ser Met Glu Arg	
20 25 30	
ata acc tct agg acg cag ctc acc ctc ctc ctc aca agg ctc ttc aag	144
Ile Thr Ser Arg Thr Gln Leu Thr Leu Leu Leu Thr Arg Leu Phe Lys	
35 40 45	
tcc acg ccc ccg ggg gcg atc ggt att gtg gtg tac ctg atc cag ggg	192
Ser Thr Pro Pro Gly Ala Ile Gly Ile Val Val Tyr Leu Ile Gln Gly	
50 55 60	
aag ctg ggg ccc gac tgg aag ggg ctg ccg gag ctg ggt gtc ggg gag	240
Lys Leu Gly Pro Asp Trp Lys Gly Leu Pro Glu Leu Gly Val Gly Glu	
65 70 75 80	
aag ctg ctt gta aag gcc ata gcc ctg gct tac aag gcc act gag gag	288
Lys Leu Leu Val Lys Ala Ile Ala Leu Ala Tyr Lys Ala Thr Glu Glu	
85 90 95	

agg gtt gag agg ctc tac aag tct gta ggc gac ctg ggg agt gtg gcc	336
Arg Val Glu Arg Leu Tyr Lys Ser Val Gly Asp Leu Gly Ser Val Ala	
100 105 110	
gag agg ctg tcg cgg gag tac cgc tcc cgg gct gcc agg gcc gtc acc	384
Glu Arg Leu Ser Arg Glu Tyr Arg Ser Arg Ala Ala Arg Ala Val Thr	
115 120 125	
ctg gag gcg ttc atg gcg gga ggg ggg gag gcg ctg act gtg agg agg	432
Leu Glu Ala Phe Met Ala Gly Gly Gly Glu Ala Leu Thr Val Arg Arg	
130 135 140	
gtt tac aac acg ctg tac agg ata gcc atg gcg cag ggt gag ggg agc	480
Val Tyr Asn Thr Leu Tyr Arg Ile Ala Met Ala Gln Gly Glu Gly Ser	
145 150 155 160	
agg gac atc aag ctt agg ctg ctg gcc ggc ctc ctg gcg gac gcc gag	528
Arg Asp Ile Lys Leu Arg Leu Leu Ala Gly Leu Leu Ala Asp Ala Glu	
165 170 175	
ccc gtg gag gcg aag tat att gtg agg ttt gtg gag ggg agg ctg agg	576
Pro Val Glu Ala Lys Tyr Ile Val Arg Phe Val Glu Gly Arg Leu Arg	
180 185 190	
gtg ggt gtt ggg gac gcg acc gtc ctc gac gcc ctc gcc atg gcc ttc	624
Val Gly Val Gly Asp Ala Thr Val Leu Asp Ala Leu Ala Met Ala Phe	
195 200 205	
ggc ggc ggg gcc cac gcg agg ccc gtt ata gag agg gcc tac aac ctc	672
Gly Gly Gly Ala His Ala Arg Pro Val Ile Glu Arg Ala Tyr Asn Leu	
210 215 220	
agg gcc gac cta ggc tac ata gcg gag gtc gtg gcc agg gag ggt gtt	720
Arg Ala Asp Leu Gly Tyr Ile Ala Glu Val Val Ala Arg Glu Gly Val	
225 230 235 240	
gat gcg ctg agg ggt gtg aag ccc cag gtc ggc gtt cct ata agg ccg	768
Asp Ala Leu Arg Gly Val Lys Pro Gln Val Gly Val Pro Ile Arg Pro	
245 250 255	
atg ctg gcc gag agg ggg agg gac ccg gct gag ata ctc agg aag gtg	816
Met Leu Ala Glu Arg Gly Arg Asp Pro Ala Glu Ile Leu Arg Lys Val	
260 265 270	
ggg ggc agg gct gtc gtc gag tat aag tac gat ggg gag agg gcg cag	864
Gly Gly Arg Ala Val Val Glu Tyr Lys Tyr Asp Gly Glu Arg Ala Gln	
275 280 285	
ata cac aag aag gac ggg gag gtc tac atc tac tcg agg agg ctt gag	912
Ile His Lys Lys Asp Gly Glu Val Tyr Ile Tyr Ser Arg Arg Leu Glu	
290 295 300	
aac ata acc agg atg ttc ccc gac gtg gtt gag atg gcg agg aag ggc	960
Asn Ile Thr Arg Met Phe Pro Asp Val Val Glu Met Ala Arg Lys Gly	
305 310 315 320	

ctc aaa gcc ggg gag gct ata gtc gag ggg gag ata gtg gcc gta gac Leu Lys Ala Gly Glu Ala Ile Val Glu Gly Glu Ile Val Ala Val Asp 325 330 335	1008
cca gac aac tat gag ata cag ccc ttc cag gtc ctc atg cag agg aag Pro Asp Asn Tyr Glu Ile Gln Pro Phe Gln Val Leu Met Gln Arg Lys 340 345 350	1056
agg aag cac gac ata cac agg gtc atg agg gag gtg ccc gtc gcc gtc Arg Lys His Asp Ile His Arg Val Met Arg Glu Val Pro Val Ala Val 355 360 365	1104
ttc ctc ttc gac gcc ctc tac gtg gac ggc gag gac ctc aca agc aaa Phe Leu Phe Asp Ala Leu Tyr Val Asp Gly Glu Asp Leu Thr Ser Lys 370 375 380	1152
ccc ctc ccc gag agg cgc agg agg ctc aag gag ata gtt gtg gag acg Pro Leu Pro Glu Arg Arg Arg Arg Leu Lys Glu Ile Val Val Glu Thr 385 390 395 400	1200
ccc ctc tgg agg ctg gcg gag tcc atc gag acc agc gac ccc gag gag Pro Leu Trp Arg Leu Ala Glu Ser Ile Glu Thr Ser Asp Pro Glu Glu 405 410 415	1248
ctg tgg acc ttc ttc ctg aag gcc ata gag gag ggg gcc gag ggc gtc Leu Trp Thr Phe Phe Leu Lys Ala Ile Glu Glu Gly Ala Glu Gly Val 420 425 430	1296
atg gtc aag gcc gtc cac agg gac tca gtc tac acc gcg ggc gta agg Met Val Lys Ala Val His Arg Asp Ser Val Tyr Thr Ala Gly Val Arg 435 440 445	1344
ggg tgg ctg tgg gtc aag ctg aag agg gat tac aag agc gag atg atg Gly Trp Leu Trp Val Lys Leu Lys Arg Asp Tyr Lys Ser Glu Met Met 450 455 460	1392
gac acg gtg gac ctc gta gtg gtg ggc gcc ttc tac ggc agg ggg aag Asp Thr Val Asp Leu Val Val Val Gly Ala Phe Tyr Gly Arg Gly Lys 465 470 475 480	1440
agg ggc ggg aag ctc agc agc ctg ctc atg gcc gcc tac gac cca gac Arg Gly Gly Lys Leu Ser Ser Leu Leu Met Ala Ala Tyr Asp Pro Asp 485 490 495	1488
agg gac gtg ttc ccc acc gtc tgc aag gtg gcc aca ggg ttc acg gac Arg Asp Val Phe Pro Thr Val Cys Lys Val Ala Thr Gly Phe Thr Asp 500 505 510	1536
gag gag ctg gac agg atg aac gag atg ctg aag aag cac atc ata ccc Glu Glu Leu Asp Arg Met Asn Glu Met Leu Lys Lys His Ile Ile Pro 515 520 525	1584
agg aag cac ccg agg gta gag tgc agg ata gag cct gac gtg tgg gtg Arg Lys His Pro Arg Val Glu Ser Arg Ile Glu Pro Asp Val Trp Val 530 535 540	1632

gag	ccc	gcc	ctc	gtg	gcg	gag	ata	ctg	ggc	gcc	gag	ctc	acc	ctc	tca	1680
Glu	Pro	Ala	Leu	Val	Ala	Glu	Ile	Leu	Gly	Ala	Glu	Leu	Thr	Leu	Ser	
545																560

cca	atg	cac	acc	tgc	tgc	ctc	aac	act	gtg	agg	ccg	ggg	gtg	ggg	ata	1728
Pro	Met	His	Thr	Cys	Cys	Leu	Asn	Thr	Val	Arg	Pro	Gly	Val	Gly	Ile	
				565					570						575	

agc	ata	agg	ttc	ccc	agg	ttc	ata	agg	tgg	agg	gac	gac	aag	agt	ccg	1776
Ser	Ile	Arg	Phe	Pro	Arg	Phe	Ile	Arg	Trp	Arg	Asp	Asp	Lys	Ser	Pro	
				580					585						590	

gag	gac	gcg	aca	aca	acc	cac	gag	ctg	ctc	gag	atg	tac	aag	agg	cag	1824
Glu	Asp	Ala	Thr	Thr	Thr	His	Glu	Leu	Leu	Glu	Met	Tyr	Lys	Arg	Gln	
		595						600							605	

ttg	agg	agg	gtt	gaa	gag	ccg	gcg	gag	cag	gtg	tag					1860
Leu	Arg	Arg	Val	Glu	Glu	Pro	Ala	Glu	Gln	Val						
			610					615								

<210> 2  
 <211> 619  
 <212> PRT  
 <213> *Aeropyrum pernix*

<400> 2

Val	Gly	Cys	Leu	Val	Leu	Ala	Ser	Ser	Ser	Gly	Gly	Val	Gly	Gly	Gly
1				5					10					15	

Asp	Met	Pro	Phe	Lys	Pro	Val	Ala	Glu	Ala	Phe	Ala	Ser	Met	Glu	Arg
			20					25					30		

Ile	Thr	Ser	Arg	Thr	Gln	Leu	Thr	Leu	Leu	Leu	Thr	Arg	Leu	Phe	Lys
		35				40						45			

Ser	Thr	Pro	Pro	Gly	Ala	Ile	Gly	Ile	Val	Val	Tyr	Leu	Ile	Gln	Gly
		50				55					60				

Lys	Leu	Gly	Pro	Asp	Trp	Lys	Gly	Leu	Pro	Glu	Leu	Gly	Val	Gly	Glu
65					70					75					80

Lys	Leu	Leu	Val	Lys	Ala	Ile	Ala	Leu	Ala	Tyr	Lys	Ala	Thr	Glu	Glu
				85				90						95	

Arg	Val	Glu	Arg	Leu	Tyr	Lys	Ser	Val	Gly	Asp	Leu	Gly	Ser	Val	Ala
			100					105					110		

Glu Arg Leu Ser Arg Glu Tyr Arg Ser Arg Ala Ala Arg Ala Val Thr  
 115 120 125

Leu Glu Ala Phe Met Ala Gly Gly Gly Glu Ala Leu Thr Val Arg Arg  
 130 135 140

Val Tyr Asn Thr Leu Tyr Arg Ile Ala Met Ala Gln Gly Glu Gly Ser  
 145 150 155 160

Arg Asp Ile Lys Leu Arg Leu Leu Ala Gly Leu Leu Ala Asp Ala Glu  
 165 170 175

Pro Val Glu Ala Lys Tyr Ile Val Arg Phe Val Glu Gly Arg Leu Arg  
 180 185 190

Val Gly Val Gly Asp Ala Thr Val Leu Asp Ala Leu Ala Met Ala Phe  
 195 200 205

Gly Gly Gly Ala His Ala Arg Pro Val Ile Glu Arg Ala Tyr Asn Leu  
 210 215 220

Arg Ala Asp Leu Gly Tyr Ile Ala Glu Val Val Ala Arg Glu Gly Val  
 225 230 235 240

Asp Ala Leu Arg Gly Val Lys Pro Gln Val Gly Val Pro Ile Arg Pro  
 245 250 255

Met Leu Ala Glu Arg Gly Arg Asp Pro Ala Glu Ile Leu Arg Lys Val  
 260 265 270

Gly Gly Arg Ala Val Val Glu Tyr Lys Tyr Asp Gly Glu Arg Ala Gln  
 275 280 285

Ile His Lys Lys Asp Gly Glu Val Tyr Ile Tyr Ser Arg Arg Leu Glu  
 290 295 300

Asn Ile Thr Arg Met Phe Pro Asp Val Val Glu Met Ala Arg Lys Gly  
 305 310 315 320

Leu Lys Ala Gly Glu Ala Ile Val Glu Gly Glu Ile Val Ala Val Asp  
 325 330 335

Pro Asp Asn Tyr Glu Ile Gln Pro Phe Gln Val Leu Met Gln Arg Lys  
 340 345 350

Arg Lys His Asp Ile His Arg Val Met Arg Glu Val Pro Val Ala Val  
 355 360 365

Phe Leu Phe Asp Ala Leu Tyr Val Asp Gly Glu Asp Leu Thr Ser Lys  
 370 375 380

Pro Leu Pro Glu Arg Arg Arg Arg Leu Lys Glu Ile Val Val Glu Thr  
 385 390 395 400

Pro Leu Trp Arg Leu Ala Glu Ser Ile Glu Thr Ser Asp Pro Glu Glu  
 405 410 415

Leu Trp Thr Phe Phe Leu Lys Ala Ile Glu Glu Gly Ala Glu Gly Val  
 420 425 430

Met Val Lys Ala Val His Arg Asp Ser Val Tyr Thr Ala Gly Val Arg  
 435 440 445

Gly Trp Leu Trp Val Lys Leu Lys Arg Asp Tyr Lys Ser Glu Met Met  
 450 455 460

Asp Thr Val Asp Leu Val Val Val Gly Ala Phe Tyr Gly Arg Gly Lys  
 465 470 475 480

Arg Gly Gly Lys Leu Ser Ser Leu Leu Met Ala Ala Tyr Asp Pro Asp  
 485 490 495

Arg Asp Val Phe Pro Thr Val Cys Lys Val Ala Thr Gly Phe Thr Asp  
 500 505 510

Glu Glu Leu Asp Arg Met Asn Glu Met Leu Lys Lys His Ile Ile Pro  
 515 520 525

Arg Lys His Pro Arg Val Glu Ser Arg Ile Glu Pro Asp Val Trp Val  
 530 535 540

Glu Pro Ala Leu Val Ala Glu Ile Leu Gly Ala Glu Leu Thr Leu Ser  
 545 550 555 560

Pro Met His Thr Cys Cys Leu Asn Thr Val Arg Pro Gly Val Gly Ile  
565 570 575

Ser Ile Arg Phe Pro Arg Phe Ile Arg Trp Arg Asp Asp Lys Ser Pro  
580 585 590

Glu Asp Ala Thr Thr Thr His Glu Leu Leu Glu Met Tyr Lys Arg Gln  
595 600 605

Leu Arg Arg Val Glu Glu Pro Ala Glu Gln Val  
610 615

<210> 3  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 3  
ggctgtctgg ttttggcttc t 21

<210> 4  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 4  
gtgaagggat ccttacacct gtcctgc 27

<210> 5  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> DNA primer

<400> 5  
taagctcgg attgtccggg aggtaaagcc ctgat 35

<210> 6  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<223> DNA primer

<400> 6

cacaggaagc tctacaggta ctccg

25

<210> 7

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA primer

<400> 7

tggatcatcag ggctttacct cccggacatt ccggacctta cggagtacct gtagagcttc

60

ctgtgcaagc

70